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Agronomic performance and morphophysiological characterization of common bean genotypes in the western region of Haiti

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Common bean is one of the world's most important food legumes and provides both nutritional security and income for low-income families in Haiti. However, common bean production in Haiti is constrained by numerous diseases and insect pests. These challenges, combined with the country's diverse agro-ecological zones, highlight the need to develop widely adapted bean varieties with strong biotic and abiotic resilience. In this study, the agronomic performance of 23 bean genotypes including advanced breeding lines and cultivars at Duvier, a highland location in western Haiti was evaluated. The variables measured included yield and yield-related traits, phenological and morphological traits, qualitative characteristics, and disease resistance. Overall, Mesoamerican bean genotypes outperformed their Andean counterparts in yield, with three genotypes (Verano, LORE 234, and PR1627-8) exhibiting superior yield-related traits. The earliest-maturing genotypes PR1423-153, LORE 234, and Local 3 reached physiological maturity within 20 days after flowering. On average, white beans were less affected by fungal and viral diseases than black beans. Overall, the agronomic performance of the breeding line PR1627-8 was comparable to that of locally adapted cultivars and represents a strong candidate for release to growers in the highland regions of Haiti.

Key words: *Phaseolus vulgaris*, yield, disease resistance, earliness, western region.

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a highly nutritious legume crop consumed by millions of people worldwide and serves as a significant source of protein (Beebe et al., 2000). Other economically important *Phaseolus* species include *Phaseolus lunatus* (lima bean), *Phaseolus*

coccineus (runner bean), and *Phaseolus acutifolius* (tepary bean). *Phaseolus* crops belong to the Fabaceae family (Yuste-Lisbona et al., 2014) and are cultivated for their edible seeds and pods.

Beebe et al. (2013). Other major crops in this family

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(include peanut (*Arachis hypogaea* L.), soybean (*Glycine max* L.), broad bean (*Vicia faba* L.), lentil (*Lens culinaris* L.), sweet pea (*Lathyrus odoratus* L.), cowpea (*Vigna unguiculata* L.), chickpea (*Cicer arietinum* L.), and alfalfa (*Medicago sativa* L.).

P. vulgaris originated in Central America and was first cultivated in Central Mexico. Extensive use of phenotypic and molecular markers has revealed considerable genetic diversity within common bean (Miklas et al., 2006; Kwak and Gepts, 2009; Blair et al., 2009), identifying two major gene pools, Andean and Mesoamerican, which were domesticated independently (Kwak and Gepts, 2009; Bitocchi et al., 2012; Schmutz et al., 2014; Ariani et al., 2016). The Mesoamerican gene pool is better adapted to lower altitudes and higher temperatures than the Andean pool (Ariani et al., 2016). These gene pools are further divided into six races based on morphological criteria and agro-ecological adaptation: Durango, Jalisco, and Mesoamerica for the Mesoamerican gene pool, and Chile, Nueva Granada, and Peru for the Andean gene pool (Blair et al., 2009).

Common bean is an important food crop in tropical, subtropical, and temperate regions of Africa, Europe, Asia, and the Americas (Wortmann et al., 2006). In 2017, over 36.4 million hectares were planted globally, producing approximately 31.4 million tons (Food and Agriculture Organization Statistical Database [FAOSTAT], 2019). The crop is widely grown in Latin America and Eastern and Southern Africa, where it contributes significantly to nutritional security and economic development (Raatz et al., 2019). Common beans are rich in protein (22 to 27% dry matter) and starch (39 to 47% dry matter) (Heuzé et al., 2015). They also contain essential vitamins and minerals, including iron and zinc, are high in soluble fiber, and have low fat content (Zargar et al., 2014; Keller et al., 2015). Additionally, common beans contain numerous bioactive compounds such as enzyme inhibitors, phytates, lectins, oligosaccharides, and phenolic substances (Zargar et al., 2014). Their polyphenolic compounds may help reduce the risk of chronic diseases such as cardiovascular disease, diabetes, colon cancer, and obesity (Zargar et al., 2017). Because of their nutritional profile, beans are often referred to as the “poor man’s meat” (Zargar et al., 2014).

In Haiti, common bean is the most important source of dietary protein, especially for resource-limited households. Due to its economic and nutritional significance, current breeding efforts aim to address production challenges such as low yield and biotic and abiotic stresses. Despite a substantial increase in demand over the last six decades, bean yield in Haiti has remained relatively stable (0.42 t ha⁻¹ in 1961 to 0.65 t ha⁻¹ in 2017) (FAOSTAT, 2019). The increase in production has therefore been achieved largely by expanding the land area under cultivation from 89,000 ha in 1961 to 171,850 ha in 2017 (FAOSTAT, 2019). Current yields in Haiti (0.6 t ha⁻¹) remain below the global average (0.86 t ha⁻¹)

(FAOSTAT, 2019).

Biotic factors limiting bean production in Haiti include viral pathogens (Bean Golden Yellow Mosaic Virus, Bean Common Mosaic Virus, Bean Common Mosaic Necrotic Virus), fungal pathogens (rust caused by *Uromyces appendiculatus*; web blight caused by *Thanatephorus cucumeris*; and root and stem rots caused by *Rhizoctonia solani*, *Fusarium solani*, and *Macrophomina phaseolina*), and bacterial blight caused by *Xanthomonas axonopodis* pv. *phaseoli* (Beaver et al., 2012). Major insect pests include leafhoppers (*Empoasca kraemerii*), leaf beetles (*Cerotoma* species), Lepidoptera species (*Hedylepta indicata* and *Etiella zinckenella*), and bruchids (*Acanthoscelides obtectus* and *Zabrotes subfasciatus*) (Beaver et al., 2012). Abiotic constraints include drought, high temperatures, nutrient deficiencies, and mineral toxicity (Colbert, 2017). These challenges, combined with the country’s diverse agro-ecological zones, underscore the need to develop widely adapted bean varieties with strong resilience to both biotic and abiotic stress.

Bean improvement in Haiti has been limited in recent decades due to insufficient investment in agricultural research and capacity building. Haitian researchers have participated in regional evaluation trials through the Bean Regional Network in collaboration with USAID’s Legume Innovation Lab, the University of Puerto Rico, and Zamorano University. The Central American Adaptation Nurseries (VIDAC) and the Central American Adaptation and Yield Trials (ECAR) evaluated red- and black-seeded improved lines with multiple disease resistance (Rosas et al., 2000; Beaver et al., 2003). Previous breeding efforts produced several locally adapted cultivars, such as Lore 234 and Salagnac, which remain widely grown by Haitian farmers. Through international collaborations, improved cultivars have been distributed across Haiti, providing disease-resistant and early maturing varieties suitable for both Central American and Haitian markets. In 2016, Quisqueya University partnered with the USAID-funded Support for Research and Development (AREA) Project, led by the University of Florida, to launch a bean breeding program aimed at developing broadly adapted, improved cultivars. The present study evaluated the agronomic performance of 23 bean genotypes, including advanced breeding lines and existing cultivars, at Duvier, a highland site in the western region of Haiti.

MATERIALS AND METHODS

Plant

Thirteen advanced breeding lines from the University of Puerto Rico, USDA-ARS, Zamorano University, the University of Nebraska, and the Legume Innovation Lab programs, along with ten cultivars sourced from local farmers in Haiti and the Organization for the Rehabilitation of the Environment (ORE), were used in this study. The genotype pool consisted of twelve black, four red-mottled, one red, one red kidney, one beige, and four white bean types (Table 1).

Table 1. General descriptive traits for the twenty-three common bean genotypes used in the study, including seed type, resistant genes, and collaborating institutions.

Genotype	Seed type	Resistant genes	Country/Institution collaboration
PR1423-99	Black	bgm1, I, bc3, CBB	Univ. of Puerto Rico
PR1423-110	Black	bgm, I, bc3, CBB	Univ. of Puerto Rico
PR1423-117	Black	bgm, I, bc3, CBB	Univ. of Puerto Rico
PR1423-153	Black	bgm, I, bc3, CBB	Univ. of Puerto Rico
XRAV-40-4 (Sankara)	Black	bgm, I, bc3, CBB	Univ. of Puerto Rico, Univ. of Nebraska, USDA-ARS, Zamorano University & National Seed Service Haiti
MEN2201-64	Black	bgm, I, bc3,	Zamorano University
PR1564-20	Black	bgm, I, bc3,	Univ. of Puerto Rico
PR1564-53	Black	bgm, I, bc3,	Univ. of Puerto Rico
PR1564-3	Black	bgm, I, bc3,	Univ. of Puerto Rico
PR1627-8	White	bgm, I, bc3,	Univ. of Puerto Rico
PR1627-10	White	bgm, I, bc3,	Univ. of Puerto Rico
PR1627-13	White	bgm, I, bc3,	Univ. of Puerto Rico
Verano	White	bgm, I, bc3,	Univ. of Puerto Rico & USDA-ARS
PR1654-1	Red Mottled	bgm, I, bc3,	Univ. of Puerto Rico
PR1654-2	Red Mottled	bgm, I, bc3,	Univ. of Puerto Rico
PR1654-3	Red Mottled	bgm, I, bc3,	Univ. of Puerto Rico
Badillo	Red Kidney		Univ. of Puerto Rico & USDA-ARS
Salagnac	Black		Farmer line
LORE 234	Black		ORE, Haiti
Local 1	Red mottled		Farmer line
Local 2	Black		Farmer line
Local 3	Red		Farmer line
Local 5	Beige		Farmer line

Experimental site and research design

The experiment was conducted at Duvier, a highland area located at latitude 18°28'48.19" N and longitude 72°14'16.43" W, at an elevation of 1083 m, approximately 7 km southeast of the commune of Port-au-Prince in the western region of Haiti (Supplementary Figure 1). The soil in this region is classified as Alfisol with a pH of approximately 7.2 (Adair et al., 2018). The trial was conducted during the first bean cropping season of the year (April to July 2018). During this period, the site received monthly rainfall ranging from 0.55 to 150.1 mm (Supplementary Figure 2) and temperatures between 23 and 29°C (Supplementary Figure 3). The experiment followed rain-fed, farmer-based production practices typical of the region. The soil was manually tilled, and seeds were sown by hand in a randomized complete block design with three replications. Each plot consisted of two rows, each 3 m long, containing 62 plants within a 3.6 m² area. In-row spacing was 10 cm, between-row spacing was 60 cm, and the distance between blocks and plots was 1 m. Weeds were controlled manually, and no supplemental irrigation was applied. Phenotypic assessment of the bean genotypes included measurement of eleven agronomic traits following the methods of Gomez et al. (2004) (Table 2). Leaf area index (LAI), defined as the ratio of leaf surface area to ground surface area, was measured using an AccuPAR LP-80 LAI meter. Disease incidence for the most common pathogens, Powdery Mildew, Bean Common Mosaic Virus (BCMV), and Bean Golden

Mosaic Virus (BGMV) was rated using the CIAT 1 to 9 scale, where 1 to 3 indicates resistance, 4 to 6 intermediate reaction, and 7 to 9 susceptibility (van Schoonhoven and Pastor-Corrales, 1987).

Data analysis

All data were subjected to analysis of variance (ANOVA) using R version 3.6.0 (R Development Core Team, 2019). Model assumptions of normality, independence of errors, and linearity were verified. Three traits, growth habit, gene pool, and disease incidence, were included as covariates to account for their influence on seed yield. The least-squares means multiple comparison test was used to detect significant differences among genotypes for the evaluated phenotypic variables. Pearson correlation coefficients were used to assess relationships among traits. Mean values of all traits were used in principal component analysis (PCA) to identify patterns of phenotypic variation.

RESULTS

Agronomic traits

Significant differences ($P < 0.05$) were observed among

Table 2. Phenological (P), morphological (M), qualitative (Q), and agronomic (A) traits for the twenty-three common bean genotypes measured in the study.

Trait	Classification	Description
Days to flowering	P	Number of days from sowing to the stage when 50% of the sampled plants have begun to flower
Physiological maturity	P	Number of days from sowing until 50% of the sampled plants have changed the color of their pods
Stem length (cm)	M	The distance from the ground surface to the tip of the main guide at flowering. Sample size: 10 plants plot ⁻¹
Pod length (cm)	M	Exterior distance from the pod apex to the peduncle. Sample size: 30 pods plot ⁻¹
Pod width (cm)	M	Distance from the right angle to the sutures as the middle of the pod. Sample size: 30 pods plot ⁻¹
Growth habit	Q	Determined according to Muñoz et al. (1993). Sample size: 10 plants plot ⁻¹
Wing petal color	Q	Determined in freshly opened flowers according to Muñoz et al. (1993). Sample size: 10 plants plot ⁻¹
Pods plant ⁻¹	A	Average number of mature pods plant ⁻¹ . Sample size: 10 plants plot ⁻¹
Seeds pod ⁻¹	A	Average number of seeds pod ⁻¹ . Sample size: 30 pods plot ⁻¹
100-seed weight (g)	A	Average 100-seed weight (at 14% moisture)
Yield per plot (kg ha ⁻¹)	A	Determined on the basis of the total number of harvested plants plot ⁻¹

genotypes for all agronomic traits (Table 3). Seed yield ranged from 0.48 to 1.24 t ha⁻¹. Except for seed weight, Mesoamerican bean types (black, white, and beige) significantly outperformed Andean types in yield, pods per plant, and seeds per pod (Supplementary Figure 4). The three highest-yielding genotypes were Verano, LORE 234, and the breeding line PR1627-8. The number of pods per plant varied significantly, ranging from 4.33 to 8.87. Seed count per pod also differed significantly ($P < 0.05$), ranging from 3.15 to 5.73. The 100-seed weight varied significantly across genotypes, ranging from 12.62 to 28.26 g (Table 3).

Phenological and morphological traits

Phenological traits evaluated included days to 50% flowering, days to 50% maturity, and earliness (defined as the interval between flowering and maturity). Significant variation ($P < 0.05$) was found across all three traits (Table 4). Days to flowering ranged from 37 to 43, while days to maturity ranged from 56 to 68. Earliness varied from 19 to 27 days after flowering. The earliest genotypes were PR1423-153, LORE 234, and Local 3, which reached physiological maturity within 19 to 20 days post-flowering (Figure 1). Significant variation was also observed in morphological traits, including stem length,

pod length, and pod width (Table 5). Stem length ranged from 25.30 to 38.67 cm, pod length from 8.02 to 11.77 cm, and pod width from 1.00 to 1.31 cm. The leaf area index (LAI) differed significantly among genotypes, ranging from 1.13 to 2.65 (Figure 2).

Qualitative traits

Three wing petal colors were observed: white, purple, and pink. Among the 23 genotypes, two had pink flowers, ten had white flowers, and eleven had purple flowers (Table 6). All white bean genotypes produced white flowers. Growth habit was either determinate or indeterminate type II, with the indeterminate type II habit being most prevalent (74% of genotypes; Table 6).

Disease resistance

Powdery mildew, BGMV, and BCMV were rated on the CIAT 1–9 scale. Genotypes showed significant variation ($P < 0.05$) in disease response (Table 7). Fourteen genotypes were resistant to powdery mildew, eight showed intermediate responses, and one was susceptible. Sixteen genotypes were resistant to BGMV, while seven exhibited intermediate responses. BCMV had the greatest

Table 3. Agronomic traits for the twenty-three common bean genotypes evaluated in Duvier, Haiti, in 2018.

Genotype	Agronomic trait				Seed type ^z
	Yield (t ha ⁻¹)	Pods plant ⁻¹	Seeds pod ⁻¹	100-seeds weight (g)	
Local5	0.83	6.47	4.67	15.87	Be
Local2	0.92	6.03	5.30	16.93	Bl
LORE 234	1.24	8.87	4.92	16.43	Bl
MEN2201-64	0.96	6.47	4.98	16.76	Bl
PR1423-110	0.78	6.10	5.27	14.11	Bl
PR1423-117	0.76	5.77	5.25	14.61	Bl
PR1423-153	0.99	6.93	5.72	14.54	Bl
PR1423-99	0.88	6.10	5.73	14.54	Bl
PR1564-20	0.82	7.20	4.48	14.34	Bl
PR1564-3	0.97	7.90	5.55	12.62	Bl
PR1564-53	1.02	7.10	5.38	15.17	Bl
Salagnac	0.94	6.97	4.67	16.57	Bl
XRAV-40-4	0.78	5.63	5.00	15.96	Bl
Local3	0.88	5.00	3.58	28.26	R
Badillo	1.01	5.40	4.31	23.55	RK
Local1	0.48	4.33	3.15	18.96	RM
PR1654-1	0.61	5.67	3.30	18.40	RM
PR1654-2	0.66	5.70	3.33	19.55	RM
PR1654-3	0.73	4.80	3.35	26.12	RM
PR1627-10	0.98	7.57	4.83	15.63	W
PR1627-13	0.94	7.47	4.95	14.77	W
PR1627-8	1.16	8.47	5.30	15.10	W
Verano	1.16	8.70	4.65	15.90	W
Mean	0.89	6.55	4.68	17.16	-
LSD (0.05)	0.55	3.07	0.75	3.04	-
CV (%)	37.56	28.58	9.73	10.8	-

^zBe: Beige, Bl: black, R: red, RM: red mottled; RK: red kidney; W: white.

impact in the field. Only seven genotypes were resistant, fourteen were intermediate, and two were susceptible. On average, white beans were the least susceptible to both fungal and viral diseases, followed by black beans (Supplementary Figure 5).

Phenotypic correlations

Several traits exhibited significant correlations (Supplementary Figure 6). Days to flowering were positively correlated with days to maturity, number of pods per plant, seeds per pod, yield, LAI, and growth habit, but were not significantly correlated with earliness. Days to maturity showed a significant positive correlation with earliness. Seed yield was positively correlated with the number of pods per plant, number of seeds per pod, and growth habit, with pods per plant showing the strongest relationship. Seed weight was positively correlated with stem length, pod length, and pod width, but negatively correlated with seeds per pod, pods per plant, days to

flowering, and growth habit. LAI was positively correlated with days to maturity, pods per plant, stem length, and days to flowering.

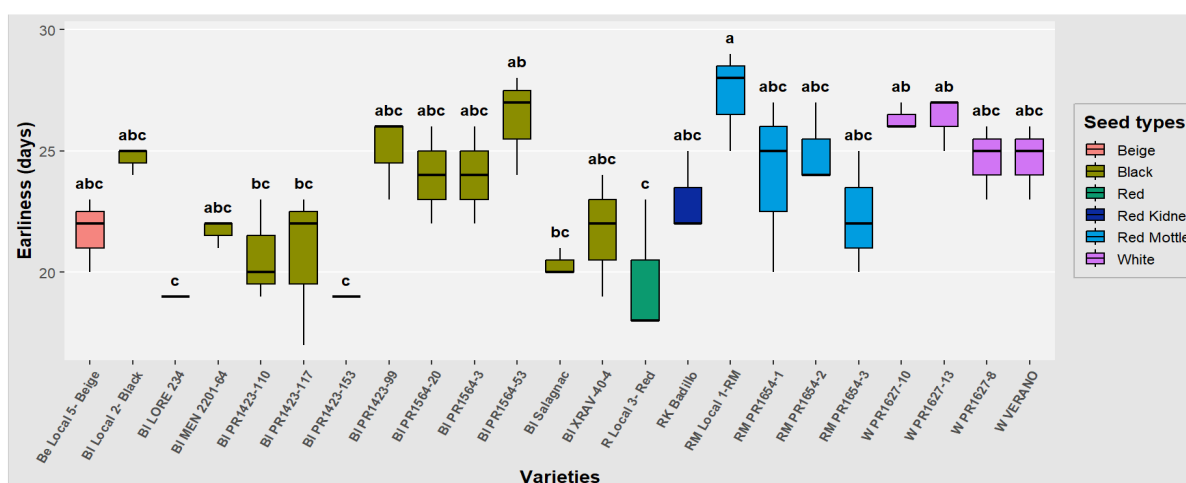
Principal component analysis

PCA revealed the proportion of phenotypic variation explained by the 11 principal components (Table 8). The first principal component (PC1) explained 53% of the total variation, distinguishing genotypes primarily based on growth habit, seed weight, seeds per pod, pods per plant, stem length, pod length, and pod width. PC2 explained 17.44% of the variation and differentiated genotypes mainly according to LAI, days to flowering, and days to maturity. PC3 accounted for 13% of the variation and separated genotypes based on seed yield, pods per plant, and pod length. Together, PC1, PC2, and PC3 explained 83.29% of the total phenotypic variation. A PCA plot using PC1 and PC2 revealed three major bean-type clusters (Supplementary Figure 7). The red-mottled

Table 4. Phenological traits for the twenty-three common bean genotypes evaluated in Duvier, Haiti, in 2018.

Genotype	Phenological trait			
	Days to flowering	Days to maturity	Earliness	Seed type ²
Local5	39.33	61.00	21.67	Be
Local2	43.00	67.67	24.67	BI
LORE 234	37.00	56.00	19.00	BI
MEN2201-64	37.33	59.00	21.67	BI
PR1423-110	41.00	61.67	20.67	BI
PR1423-117	40.33	61.00	20.67	BI
PR1423-153	40.00	59.00	19.00	BI
PR1423-99	40.67	65.67	25.00	BI
PR1564-20	41.00	65.00	24.00	BI
PR1564-3	42.33	66.33	24.00	BI
PR1564-53	41.67	68.00	26.33	BI
Salagnac	41.67	62.00	20.33	BI
XRAV-40-4	37.33	59.00	21.67	BI
Local3	37.00	56.67	19.67	R
Badillo	41.00	64.00	23.00	RK
Local1	37.00	64.33	27.33	R M
PR1654-1	37.67	61.67	24.00	R M
PR1654-2	39.00	64.00	25.00	R M
PR1654-3	39.67	62.00	22.33	R M
PR1627-10	42.00	68.33	26.33	W
PR1627-13	41.33	67.67	26.33	W
PR1627-8	42.33	67.00	24.67	W
Verano	41.33	66.00	24.67	W
Mean	40.04	63.17	23.13	
LSD (0.05)	1.72	2.65	3.14	
CV (%)	2.62	2.56	8.26	

²Be: Beige, BI: black, R: red, RM: red mottled, RK: red kidney, W: White. Means followed by the same letter are not significantly different.

**Figure 1.** Earliness of the 23 common bean genotypes.

genotypes formed a distinct cluster characterized by high seed weight, pod length, and pod width. Black beans

formed the largest and most variable cluster across traits, including seed yield, pods per plant, seeds per pod, days

Table 5. Morphological traits for the twenty-three common bean genotypes evaluated in Duvier, Haiti, in 2018.

Genotype	Morphological trait			
	Stem length (cm)	Pod length (cm)	Pod width (cm)	Seed type ^z
Local5	34.59	8.94	1.11	Be
Local2	31.74	8.89	1.09	Bl
LORE 234	33.72	8.94	1.10	Bl
MEN2201-64	26.42	8.75	1.08	Bl
PR1423-110	27.43	8.55	1.00	Bl
PR1423-117	27.08	8.44	1.05	Bl
PR1423-153	25.30	8.91	1.04	Bl
PR1423-99	26.35	9.07	1.06	Bl
PR1564-20	27.34	8.02	1.08	Bl
PR1564-3	28.80	8.92	1.08	Bl
PR1564-53	26.24	8.49	1.13	Bl
Salagnac	38.22	9.37	1.17	Bl
XRAV-40-4	27.83	8.55	1.06	Bl
Local3	34.21	11.24	1.31	R
Badillo	38.67	11.77	1.24	RK
Local1	33.29	9.08	1.17	R M
PR1654-1	34.69	9.86	1.19	R M
PR1654-2	35.88	9.83	1.21	R M
PR1654-3	34.19	9.83	1.24	R M
PR1627-10	26.70	8.07	1.13	W
PR1627-13	26.38	8.10	1.10	W
PR1627-8	26.56	8.85	1.10	W
Verano	28.25	8.05	1.13	W
Mean	30.43	9.07	1.13	
LSD (0.05)	7.06	0.86	0.15	
CV (%)	14.12	5.76	8.16	

^zBe: beige, Bl: black, R: red, RM: red mottled, RK: red kidney, W: White.

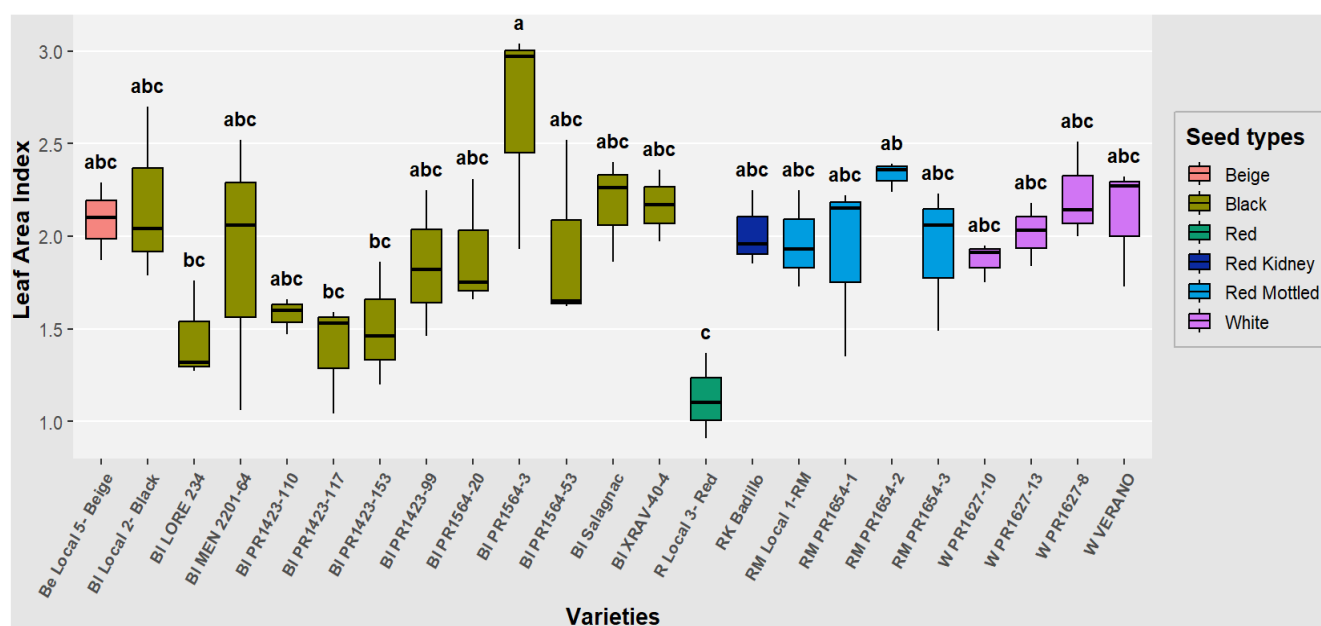


Table 6. Qualitative traits for the twenty-three common bean genotypes evaluated in Duvier, Haiti, in 2018.

Genotype	Growth habit	Wing petal color	Seed type
Local5	Indeterminate type II	white	Beige
Local2	Indeterminate type II	purple	Black
LORE 234	Indeterminate type II	purple	Black
MEN2201-64	Indeterminate type II	purple	Black
PR1423-110	Indeterminate type II	purple	Black
PR1423-117	Indeterminate type II	purple	Black
PR1423-153	Indeterminate type II	purple	Black
PR1423-99	Indeterminate type II	purple	Black
PR1564-20	Indeterminate type II	purple	Black
PR1564-3	Indeterminate type II	purple	Black
PR1564-53	Indeterminate type II	purple	Black
Salagnac	Indeterminate type II	pink	Black
XRAV-40-4	Indeterminate type II	purple	Black
Local3	Determinate	white	Red
Badillo	Determinate	white	Red kidney
Local1	Determinate	white	Red mottled
PR1654-1	Determinate	pink	Red mottled
PR1654-2	Determinate	white	Red mottled
PR1654-3	Determinate	white	Red mottled
PR1627-10	Indeterminate type II	white	White
PR1627-13	Indeterminate type II	white	White
PR1627-8	Indeterminate type II	white	White
Verano	Indeterminate type II	white	White

to maturity, and LAI. White beans formed a more compact cluster with comparatively low variability. Beige and red bean genotypes were closely associated with the Mesoamerican and Andean gene pools.

DISCUSSION

Significant variation was observed among the 23 common bean genotypes for the majority of measured traits. Overall, Mesoamerican genotypes outperformed Andean genotypes in every agronomic trait except seed weight. This difference in agronomic performance between the two gene pools is expected and is well documented in the literature (Singh et al., 1991; White and Gonz  les, 1990; White et al., 1992; Sexton et al., 1994). As anticipated, growth habit and disease incidence had a significant impact on seed yield. When these variables were included as cofactors in the model, yield variation among genotypes was no longer significant. Yield showed strong positive correlations with the number of pods per plant and the number of seeds per pod, indicating that these traits may serve as reliable indicators for indirect selection of dry bean seed yield. Similar positive correlations have been reported previously (Mebratu et al., 1991). These findings are expected, as the number of pods per plant and the

number of seeds per pod are known to be major determinants of seed yield in common bean (Ambachew et al., 2015; Mebratu et al., 2001). The association among these three traits may imply pleiotropy or genetic linkage among underlying loci (Dilday et al., 1990), enabling simultaneous improvement of the traits (Ambachew et al., 2015).

Significant negative correlations were observed between seed weight and both the number of pods per plant (-0.31^*) and the number of seeds per pod (-0.59^*). This result supports earlier observations that yield differences between Andean and Mesoamerican gene pools are primarily influenced by seed size (White and Gonz  les, 1990). Genotypes also differed significantly in phenological and morphological traits. The genotype LORE 234 (black-seeded) showed the fewest days to flowering and maturity among the Mesoamerican types, whereas Local 3 (red-seeded) performed best for these traits within the Andean gene pool. These cultivars could be valuable sources for enhancing earliness in Haiti's bean breeding programs. As expected, the days to flowering and days to maturity were positively correlated (Zeven et al., 1999). However, the days to flowering were not significantly associated with overall earliness, likely due to differences in growth habit. Indeterminate genotypes may flower early but take longer to reach physiological maturity than determinate types. Thus, the

Table 7. Disease score for mildew, BGMV, BCMV across 23 bean genotypes evaluated in Duvier, Haiti, in 2018.

Varieties	Mildew	Category ^z	BGMV	Category ^z	BCMV	Category ^z
Local5	3.00	R	3.67	I	6.00	I
Local2	3.00	R	1.00	R	5.00	I
LORE 234	3.00	R	5.00	I	5.67	I
MEN 2201-64	4.00	I	2.67	R	3.00	R
PR1423-110	3.33	R	6.00	I	2.33	R
PR1423-117	3.67	I	5.33	I	2.67	R
PR1423-153	3.33	R	6.00	I	1.00	R
PR1423-99	3.00	R	4.67	I	6.00	I
PR1564-20	2.00	R	1.67	R	5.67	I
PR1564-3	2.67	R	1.33	R	6.00	I
PR1564-53	2.00	R	1.67	R	5.33	I
Salagnac	3.00	R	2.00	R	6.00	I
XRAV-40-4	2.67	R	2.33	R	5.00	I
Local3	8.00	S	5.33	I	6.33	I
Badillo	6.00	I	1.67	R	4.67	I
Local1	5.67	I	2.33	R	6.33	I
PR1654-1	5.00	I	1.33	R	6.67	S
PR1654-2	5.33	I	1.33	R	6.00	I
PR1654-3	6.00	I	1.67	R	6.67	S
PR1627-10	2.33	R	2.00	R	2.33	R
PR1627-13	3.67	I	1.67	R	4.00	I
PR1627-8	2.33	R	1.33	R	1.33	R
Verano	2.67	R	1.00	R	2.00	R
Mean	3.72		2.74		4.61	
LSD(0.05)	1.35		1.31		2.05	
CV(%)	22.16		29.05		27.03	

^z R= resistant, I= intermediate, S= susceptible.

Table 8. Principal component analysis showing the proportion of the phenotypic variation explained by each trait across the twenty-three common bean genotypes evaluated in Duvier, Haiti, in 2018.

Parameter	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Variation explained (%)	52.99	17.44	12.86	6.52	4.95	2.52	1.4	0.72	0.46	0.1	0.06
Days to flowering	-0.25	-0.45	-0.11	0.44	0.2	-0.4	-0.11	0.53	-0.08	0.07	-0.16
Days to maturity	-0.17	-0.58	0.16	0.31	-0.28	0.01	0.19	-0.54	0.21	-0.19	0.17
Stem length(cm)	0.32	-0.19	-0.2	-0.37	0.37	-0.61	-0.03	-0.3	0.23	0.12	0.13
Pod length (cm)	0.34	-0.08	-0.31	0.18	0.45	0.26	0.45	0.02	-0.2	-0.5	-0.01
Pod width (cm)	0.35	-0.23	-0.26	0.05	-0.3	0.02	-0.2	-0.22	-0.69	0.28	-0.12
Pods plants ⁻¹	-0.31	-0.05	-0.42	-0.35	-0.37	-0.13	0.32	0.26	-0.16	-0.12	0.49
Seeds pod ⁻¹	-0.36	0.12	-0.14	0.23	0.47	0.23	0	-0.24	-0.15	0.48	0.44
Seed weight (g)	0.37	-0.03	-0.23	0.26	-0.12	0.19	-0.54	0.19	0.32	-0.13	0.5
Yield (t ha ⁻¹)	-0.22	0	-0.69	-0.01	-0.08	0.21	-0.07	-0.16	0.38	0.1	-0.48
Leaf Area Index	-0.09	-0.56	0.15	-0.54	0.23	0.48	-0.21	0.17	-0.01	0.03	-0.02
Growth Habit	-0.39	0.14	-0.06	-0.08	0.15	-0.16	-0.52	-0.27	-0.29	-0.59	-0.02

number of days from flowering to maturity is a more reliable measure of earliness than days from sowing to flowering. Days to flowering showed positive correlations

with both the number of seeds per pod and the number of pods per plant, reflecting known phenological differences between Mesoamerican and Andean gene pools. Stem

length, pod length, and pod width all exhibited positive and significant correlations, with the strongest association observed between pod length and pod width. Similar relationships have been reported previously (Zeven et al., 1999). Longer and wider pods were also associated with higher seed weight, consistent with the expectation that large-seeded bean types require larger pod structures. White bean genotypes exhibited only white flowers, consistent with earlier findings. In contrast, white flowers occurred in other seed-coat types but were absent in black beans. Indeterminate growth habit was observed in 74% of the genotypes (primarily Mesoamerican), while the remaining 26% (primarily Andean) showed determinate growth. As documented in prior research, growth habit showed a positive association with pods per plant and seeds per pod (Kornegay et al., 1992).

Significant differences in disease incidence were also detected among genotypes. Several breeding lines (PR1423-99, PR1423-110, PR1423-153, PR1564-20, PR1564-3, PR1564-53, PR1627-10, and PR1627-8) showed resistance to powdery mildew and may serve as parental sources in breeding programs. For BGMV, nine of the 13 breeding lines were resistant, and five showed intermediate resistance, likely due to the presence of the *bgm1* gene. The *bgm1* gene, located on Pv03, provides resistance to chlorosis caused by BGMV infection (Urrea et al. 1996; Velez et al., 1998; Blair et al., 2007). Eleven of the breeding lines (74%) displayed intermediate to high resistance to BCMV, consistent with the presence of the *I* gene on Pv02 (Vallejos et al., 2000) and the *bc-3* gene on Pv06 (Johnson et al., 1997), which together provide resistance to all known BCMV and BCMNV strains (Mukeshimana et al., 2005). Principal component analysis showed distinct clustering by bean type, with red mottled genotypes forming a separate cluster characterized by high seed weight, long pods, and wide pods, while black and white beans formed their own distinct clusters.

Conclusions

The national average yield of common bean in Haiti is approximately 0.6 t ha⁻¹, which is below the global average of 0.86 t ha⁻¹, highlighting the need for accelerated development and adoption of improved bean genotypes. Among the evaluated lines, the advanced breeding line PR1627-8 (white-seeded) demonstrated superior performance in yield and disease resistance, making it a strong candidate for release to growers. Additionally, the cultivars LORE 234 (black-seeded) and Local 3 (red-seeded), which are already grown by farmers, represent valuable sources of earliness for breeding programs. Based on phenotypic relationships, the number of pods per plant and the number of seeds per pod appear to be useful traits for the indirect selection of seed yield in common bean. Given that the data were collected from a single season and location, further multi-environment trials are needed to confirm these results.

The significant differences detected among genotypes for most traits indicate strong potential for yield improvement through targeted breeding. Future efforts should prioritize traits such as yield potential, disease resistance, and early maturity while ensuring that newly developed cultivars are well adapted to Haiti's diverse agro-ecological environments. Strengthening the seed value chain is also essential to ensure that farmers have timely access to affordable, high-quality seed. Investments should therefore extend beyond breeding to support local seed enterprises, distribution networks, and extension services to promote widespread adoption of improved cultivars.

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CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

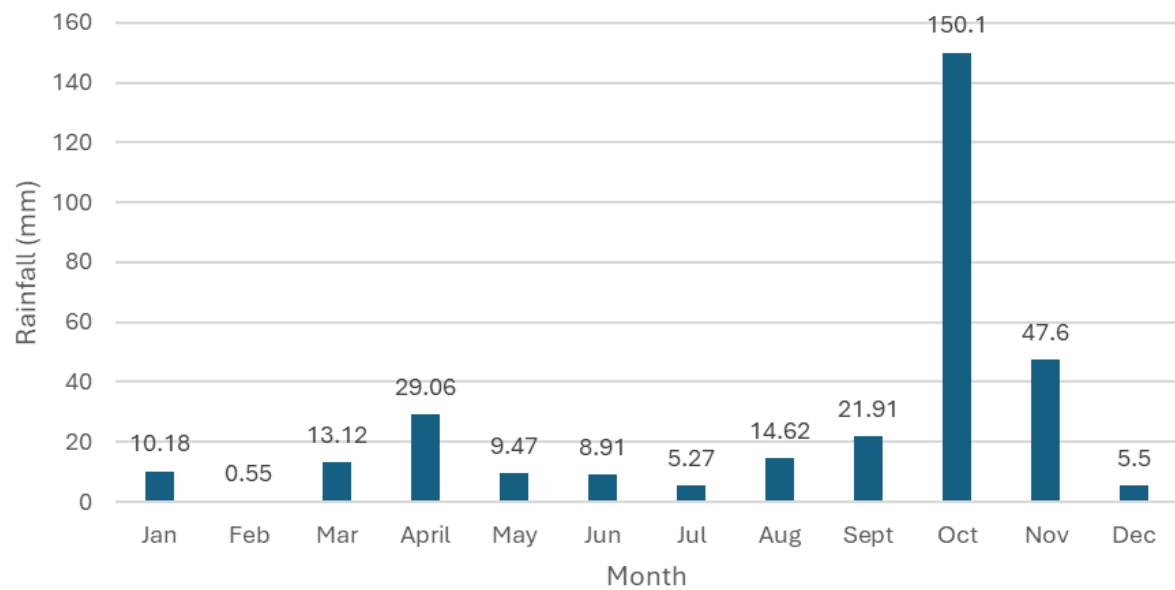
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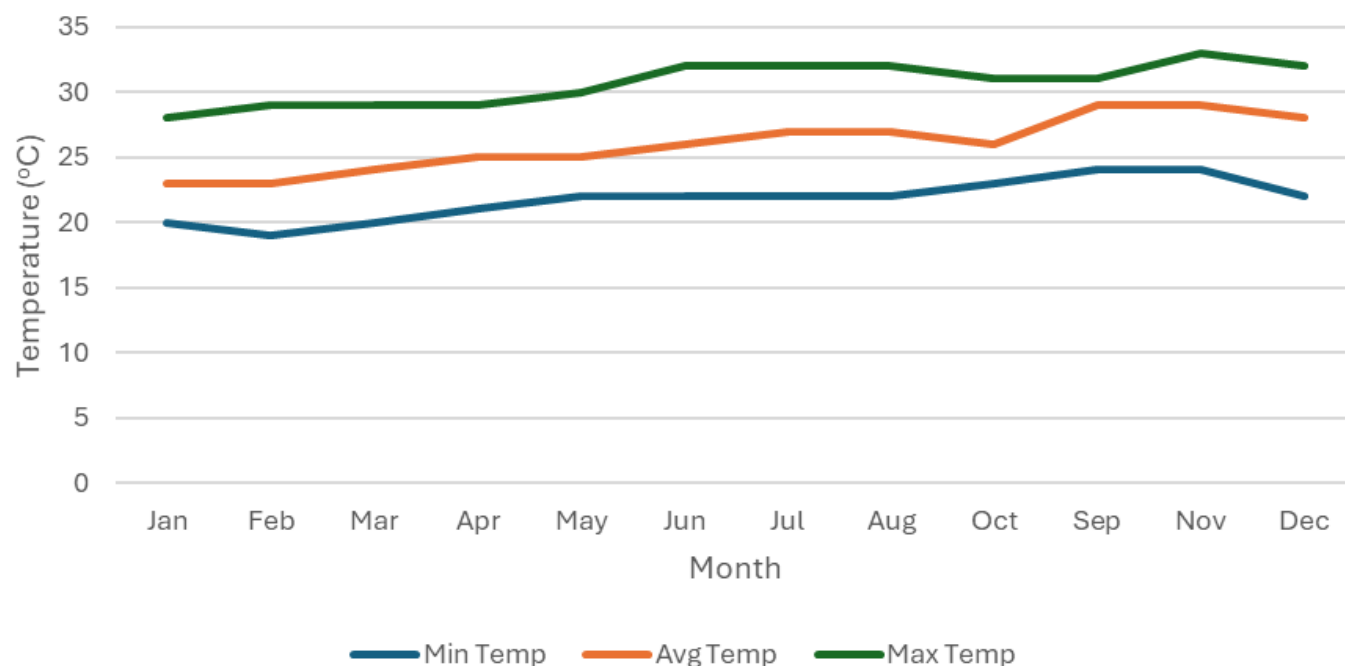
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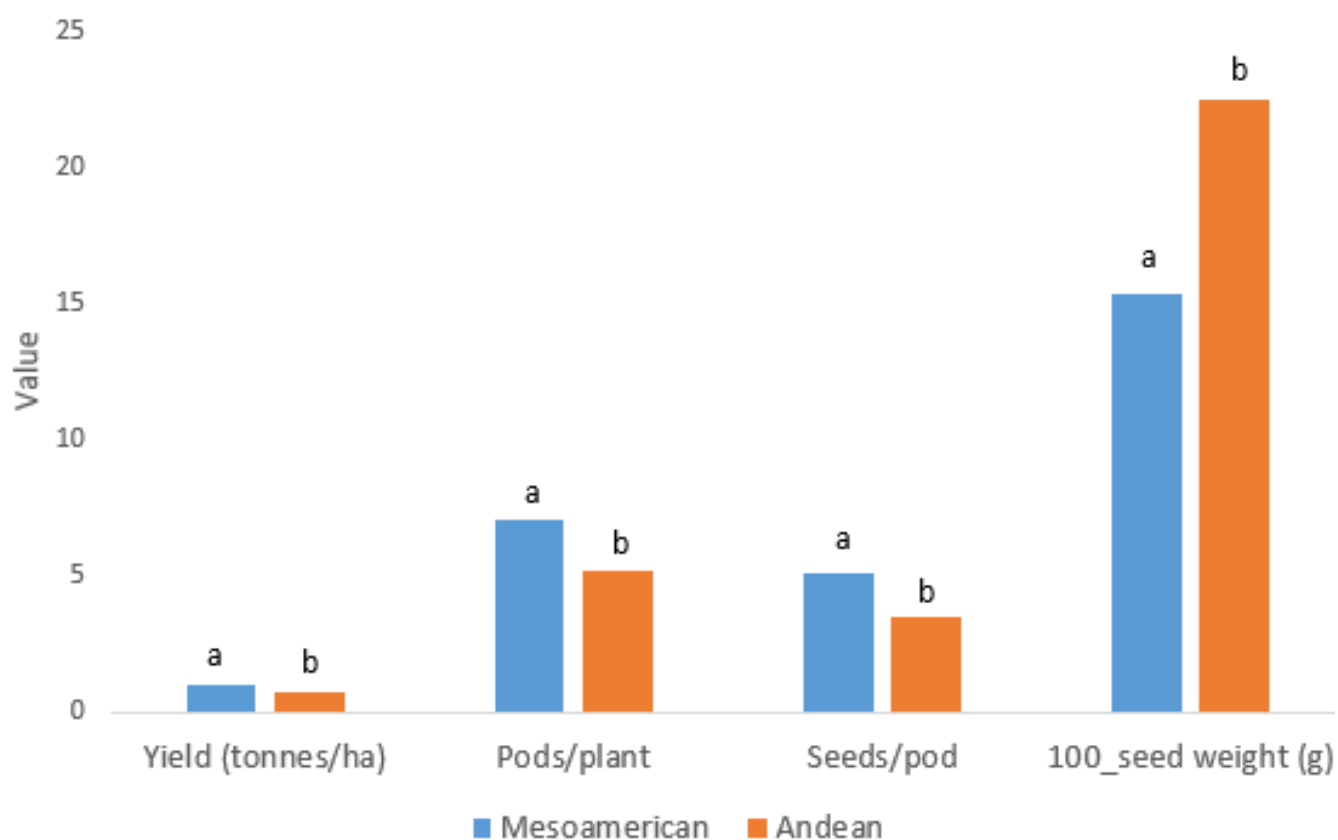
Supplementary Figure 1. Location of the experimental site.



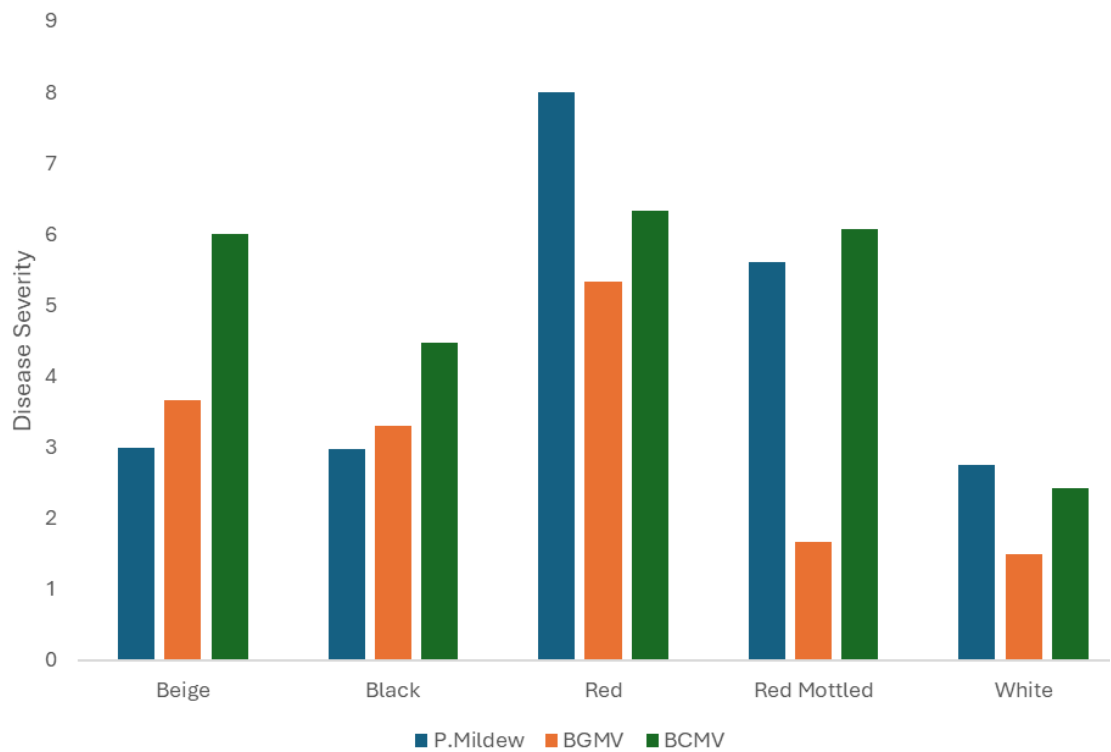
Supplementary Figure 2. Rainfall of experimental site.
Source: Worldweatheronline.com.



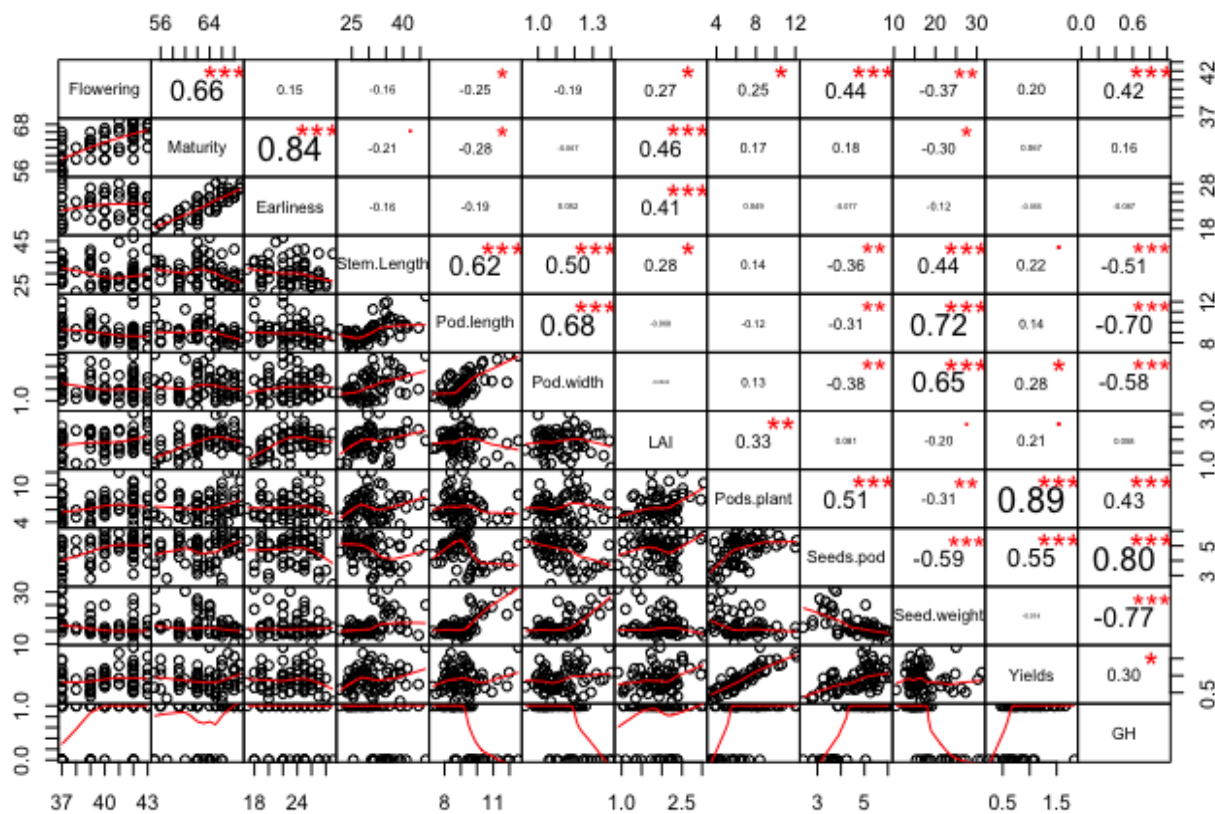
Supplementary Figure 3. Temperature of the experimental site. Data from Worldweatheronline.com. Source: Worldweatheronline.com.



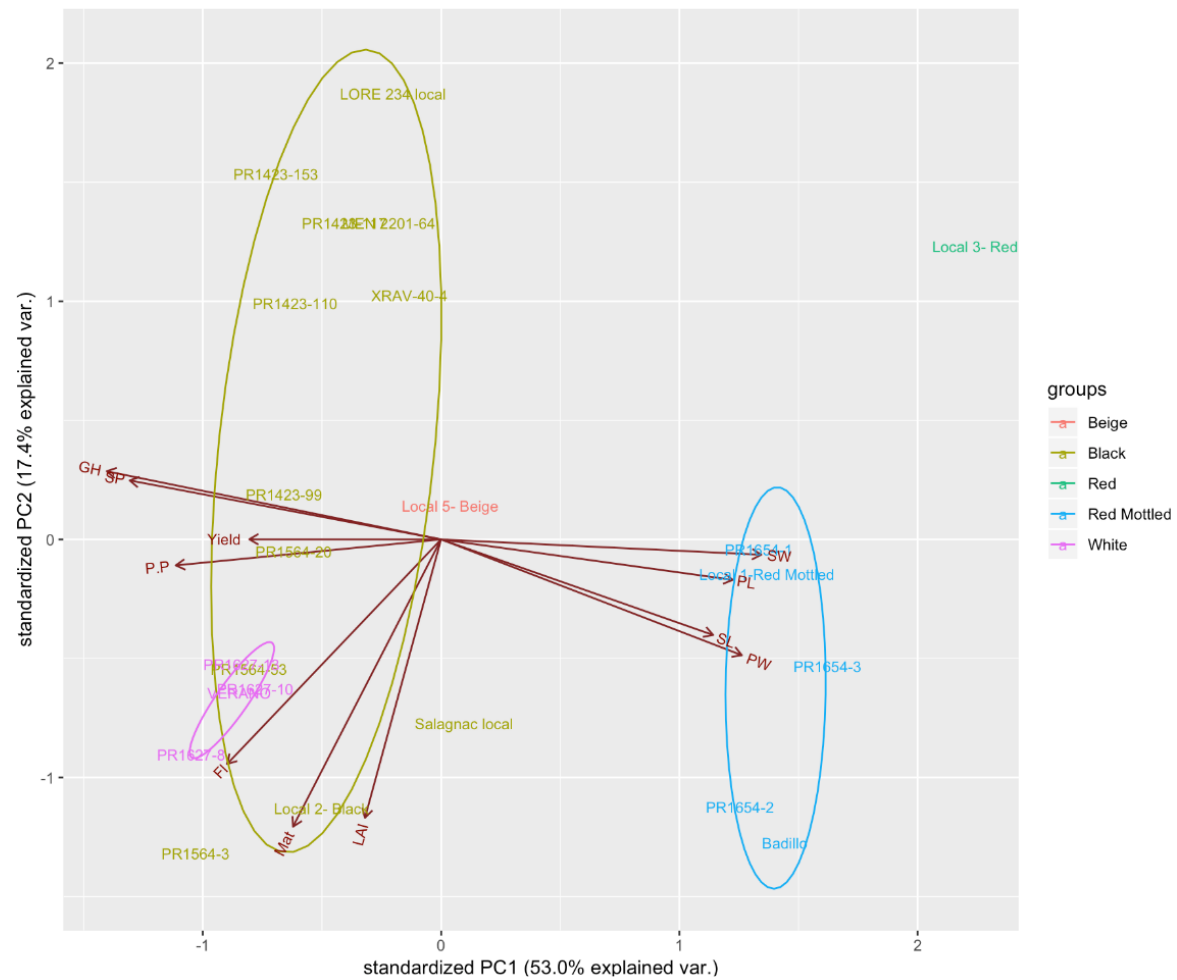
Supplementary Figure 4. Variation in yield and yield components between cultivars of Mesoamerican and Andean gene pool in the current study.



Supplementary Figure 5. Disease severity by common bean type.



Supplementary Figure 6. Phenotypic correlations between the traits measured in the study.



Supplementary Figure 7. Principle component analysis for the phenotypic traits measured in the study.